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OBL-GA based FCM with level sets for automatic GBM tumor segmentation in MR Images

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Abstract— **This paper presents an automatic method for the segmentation of Glioblastoma multiforme(GBM) tumors from MRI images. The global search ability of Genetic Algorithm (GA) to optimize the Fuzzy C-means (FCM) clustering algorithm to obtain better clustering center. But the prematurity problem of GA itself has bad effects on the whole clustering. Therefore, in order to optimize the traditional GA-FCM algorithm's clustering effect, in this work, we introduce the Opposition-based learning mechanism into GA, to construct an OBL-Genetic Algorithm (OBL-GA). The improved algorithm forms the next generation of evolutionary population by selecting the superior individuals in the collection of the sub generation and reverse sub generation, to increase the population diversity, and final to overcome the prematurity problem of GA. Then applying the improved algorithm to FCM, which gives better results and then resultant image, is applied with level sets, to exact delineation of GBM tumor. The validation is performed on a labeled BRATS data set. Our segmentation results are highly accurate, and compare favorably to the state of the art.**

Keywords-Fuzzy-c means,Glioblastoma multiforme,Segmentation,Genetic Algorithm,Opposition based learning,MRI.

I. INTRODUCTION

MRI is the best imaging technique for examination of brain, it is widely used in the diagnosis of brain diseases [1], follow-up of patient [2], evaluation of therapy [3] and human brain mapping [4]. MRI has number of advantages over other methods, in particular it is non-invasive and highly sensitive to the contrast acquisition. Hence, it shows a good spatial resolution and an very good performance when visualizing different tissues of human body. In many practical cases, MRI is associated to conventional imaging of gliomas, Gliomas are the most common type of primary brain tumor of the central nervous system. They come mainly from glial cells in the brain. According to the World Health Organization (WHO), there are two types of gliomas. The first type concerns what it is called low-grade gliomas (grade I and grade II), such as astrocytomas or oligodendrogliomas. These tumors account 50% of gliomas and the medium age of patients affected is around forty years. They are characterized by irregular contour, shapes and a continuous growth before the malignant transformation occurs. The life expectancy of people diagnosed with this type of glioma is of several years, and intensive treatment is being administered in order to prevent malignant progression. The second category of gliomas concerns the high grade gliomas (grade III and grade IV). The most common malignant of this type of gliomas is called the glioblastoma (GBM). In this case, the median life expectancy of patients is less than 12 months. Despite the considerable progress in research on gliomas and the availability of technical and material resources established for the management of patients with gliomas, the diagnosis of these tumors remains insufficient. Precisely, the main difficulty consists in the operation and interpretation of these images by neurosurgeons. In fact, the segmentation of gliomas on MRI images is one of the most crucial procedures in the surgical and treatment planning. Currently, this process is performed manually in clinical practice. In addition to being time consuming, manual gliomas delineation is unreliable and depends on the individual operator.

Recent reviews on brain tumor segmentation are on both supervised and unsupervised methods and other methods are soft computing and combination of different methods. Supervised approach applied for multiparametric MR datasets to segment health and pathological tissues [5,6]. The presence of artifacts create problem in image enhancement and reduces the accuracy of segmentation[7]. Recently, both supervised and unsupervised segmentation methods for identification of brain tissue structures have been proposed. Furthermore, the supervised approaches are limited to the size and quality of the dataset, among other limitations such as the over-fitting to the training corpus[8].Automatic tissue or tumor segmentation based on multi-spectral data analysis [9, 10], neural networking [11,

12], support vector machines [13,14] and knowledge-based fuzzy c-means (FCM)clustering techniques [15–16] all show great promise. [17]Uses ANFIS, Genetic and FCM algorithms in a sequence which strengthen individual weakness and gets good results but it's computational complexity is high. The potential advantages of automatic tumor segmentation include removal of intra- and inter-observer variations, time efficiency and standardized criteria's for tumor characterization.

Therefore, in order to better optimize the clustering results of the traditional GA-FCM algorithm, this paper introduces the concept of Opposition-based Learning (OBL) into the traditional GA to improve the prematurity problem of it, then producing an OBL-Genetic Algorithm (OBL-GA), and applying the improved algorithm to FCM algorithm. This work shows that this method can effectively improve the efficiency of the algorithm, and get better clustering results. Finally level sets is used for exact GBM tumor segmentation and boundary tracking**.** The rest of this paper is organized as follows: Section 2 presents the Fuzzy C-Means clustering. Section 3 presents the OBL-GA Algorithm, Section 4 presents FCM clustering algorithm with level sets based on OBL-GA, Section 5 gives the Experimental results and finally Section 6 report conclusions.

II. Fuzzy C-Means Clustering

The Fuzzy C-Means (FCM) clustering algorithm was first introduced by Dunn and later was extended by Bezdek. The algorithm is an iterative clustering method that produces an optimal c partition by minimizing the weighted within group sum of squared error objective function J_{FCM}.

$$J_{FCM}=\sum_{k=1}^{n}\sum_{i=1}^{c}(u_{ik})^{q}\, d^2(x_k,v_i)$$

The FCM algorithm in its original form assigns a membership value to each pixel for all clusters in the image space. For an image I with set of grayscales x_i at pixel i(i = 1,2,....,N), $X = \{x_1,x_2,....,x_N\} \subset R^k$ in k-dimensional space and cluster centers $v = \{ v_1,v_2,....,v_c\}$ with c being a positive integer (2< c <N), there is a membership value $u_{ij}$for each pixel i in the j^{th}cluster (j = 1,2,...,c). The objective function of the FCM algorithm is [18]

$$J_{FCM} = J(U, A1, A2 \dots AC) = \sum_{i=1}^{N}\sum_{j=1}^{c} u_{ij}^{m} \|x_i - v_j\|^2 \quad (1)$$

where m is a weighting exponent to the degree of fuzziness ,that is ,m>1 ,and $\|x_i - v_j\|^2$ is the grayscaleeuclidean distance between pixel i and center v_j. the membership u_{ij}should be constrained to the following:

$$\forall i \in [0, N] , j \in [1, c]:$$

$$\sum_{j=1}^{c} u_{ij} = 1, u_{ij} \in [0,1], 0 \le \sum_{i=1}^{N} u_{ij} \le N \quad (2)$$

The membership function and cluster centers are updated iteratively in an alternating process known as alternate optimization. The membership function and cluster centers are

$$u_{ij}=\frac{1}{\sum_{k=1}^{c}\left(\|x_i-v_j\|^2/\|x_i-v_k\|^2\right)^{1/(m-1)}}$$

$$v_j = \frac{\sum_{i=1}^{N} u_{ij}^{m}\, x_i}{\sum_{i=1}^{N} u_{ij}^{m}} \quad (3)$$

As the objective function in (1) does not include any local information, the original FCM is very sensitive to noise and the accuracy of clustering in the presence of noise and image artifacts will decrease.

III. OBL-GA Algorithm

A genetic algorithm is an iterative procedure that involves a population of individuals, each one represented by a finite string of symbols, known as the genome, encoding a possible solution in a given problem space. GA is used to generate the global optimal solution after the initialization of the population. When the certain stopping rule is satisfied, the search stops, and the optimal solution set is called the population denoted as (t). Here, t represents the evolution of the algebra, that is to say that the current group of (t) produce the next generation of group $(t+1)$ after iterative operation. When the group falls into local extreme value, the iterative operation could be stagnant, and then causing premature convergence. After the occurrence of premature phenomenon, the current search area of the population would be difficult to cover the global optimal solution [19]. The biggest reason for the problem of the GA's easy to be premature, is that in the process of evolution, the speed of selecting offspring is too fast, and the speed of generating new individuals is too slow, which could lead to the rapid loss of population diversity. What's more, it makes the optimal solution could not be covered in the next generation of evolutionary groups. In the traditional GA, the generation of new individuals is produced by the crossover and mutation operators. In general, we can speed up the production of new individuals by increasing the probability of crossover and mutation. But if the new individual's production rate is too fast, it would lead to the higher population diversity. This can lead to the loss of the solution which is saved by the individual. Then it could be very difficult to achieve the final convergence, or it would make the convergence rate too slow. Therefore, in this paper we introduce the concept of OBL mechanism to ensure that the population diversity is increased while maintaining the

stability of the population, in order to improve the shortcomings of traditional GA's precocity.

3.1 OBL-GA Algorithm:

In order to overcome the shortcoming of traditional GA's easy to be premature, and to improve the optimization performance, in this paper we apply the concept of OBL to the traditional GA, producing a new kind of optimization algorithm–OBL-GA. In order to balance the diversity and stability of individuals in the population, we select a number of best individuals from the collection of current population and its reverse population as the next generation of input population. According to the relevant concepts of OBL, the reverse steps of the algorithm are:

Step1: Update the search area space [a(t), b(t)] for the current evolutionary community P(t).

Step2: Generate the corresponding reverse group P(t)′ according to the relevant OBL formula.

Step3: Calculate the target function value of the offspring, and then select s best individuals from P(t) U P (t)′ to compose new current group P(t+1) as the next generation of input population.

(1)Coding method

In popular terms, the code means that we could transform the real variables to the object that can be used by GA directly through a mechanism. In this paper, the classical binary coding is used to encode the original population, and each chromosome is composed of 0 and 1 strings. The value of the allele indicates the selection of the corresponding position of the individual. If No i bit is 1, which indicates that the individual is selected; if No I bit is 0, which indicates that the individual is not selected.

(2)The fitness function

For solving the problem, it is usually judged by calculating the fitness value to select the solution quality. The fitness value of each individual in the population is calculated according to the preset fitness function. As usual, the fitness function of the traditional GA-FCM algorithm is the same objective function J as the FCM clustering algorithm. But this kind of setting makes the degree of membership matrix need to be used every time to calculate the fitness value, which leads to the need of consuming a lot of time to update the membership matrix. This greatly reduces the efficiency of the algorithm. In order to solve the problem, in this paper we uses the new fitness function which is mentioned in the literature [20]. The function is defined as follows:

$$F = 1/(R \times f^{2}(t)) \quad (4)$$

$$f(t) = 1 - a \times \exp(-t / b) \quad (5)$$

Among them, t indicates an algebra of population evolution a/b indicate constant.

$$R = \sum_{j=1}^{n}(\sum_{i=1}^{c}(d(x_{j,},A_i))^{1/(1-m)})^{1/(1-m)} \quad (6)$$

In the formula d(x_j,A_i) refers to the Euclidean distance between the sample x_j and the cluster center A_i, m indicates the ambiguity parameter.

(3)Selection, crossover and mutation

Selection refers to selecting outstanding individuals from the current population as the father and inheriting good gene to the offspring [21]. In order to ensure the excellent individuals not to be destroyed by crossover, mutation and other evolutionary operations, in this paper we uses random sampling method to select the offspring. The random sampling method is similar to the roulette selection method, and the difference is that there is only one rotation of the disc in the whole process. Stochastic universal sampling method uses the rotating pointer evenly distributed and the number of the pointer is right equal to the population size [22]. It selects individuals according to the same distance and the best individual in the population is directly elected to the next generation. And then choosing N parent individuals to crossover and mutation, in this paper, we use simple single point crossover and discrete variation.

IV FCM clustering algorithm with level sets based on OBL-GA

According to the above introduction, the FCM clustering algorithm based on OBL-GA is described as follows:

Step1: Setting the initial parameters (fuzzy parameter λ = 3, maximum genetic algebra MAXGEN=50, crossover probability P_c = 0.7, mutation probability Pm = 0.01).

Step2: Population random initialization, selecting m individuals as the initial population.

Step3: Calculating the fitness value of the individual in the population according to the fitness function, and comparing with the set threshold value.

Step4: Performing the operation for each individual in the population according to the probability of the selection, crossover and mutation operation, and forming a new generation P(t).

Step5: Performing the reverse operation for the generation P(t), and forming its reverse population P(t)′. Selecting s individuals as the next generation of input population (t+1) from the collection of P(t) U $P(t)'$.

Step6: If the iterative performance of the twice algorithm is not improved or the maximum number of iterations has been reached, then end the operation, and output the result of the optimal clustering center. Otherwise go back to the Step3 to continue.

Step7: Applying the level set method [23] for the GBM tumor extraction

V RESULTS AND ANALYSIS

In this section, The performance of the proposed method is compared with FFCM[24], K-means[25], conventional FCM[26],], GA-FCM[27],PSO-FCM[28]. We present the experimental results on The Brain Tumor Image Segmentation (BRATS) Benchmark dataset [29] is used. In this experiment , The BRATS dataset is publicly available through the annual Medical Image Computing and Computer Assisted Intervention (MICCAI) Society brain tumor segmentation challenge [29]. The dataset consists of 30 fully anonymized multi-contrast MR scans of glioma patients. We use 22 images of the FLAIR and T1C MRI modality. Fig.2(a),Fig.3(a),Fig.3(a),and Fig.3(a) are DS1(Dataset1), DS2, DS3 and DS4 respectively. The experiments were performed on a 2.99 GHz Intel Core 2 Duo processor, Windows XP with 3.21 GB RAM, using Matlab R2012a.

Segmentation results on BRATS data set are shown in Fig. 3. The algorithms K-Means (Fig.2(b)), FCM(Fig.2(c)), FFCM(Fig.2(d)) ,PSO-FCM(Fig.2(e), PSO-FCM(Fib.2(f)), proposed method (Fib.2(g) and proposed method with level sets(Fig.2(h)). From these results it is obvious that K-Means, FCM, FFCM. We can see that the algorithm in this paper improve the accuracy of FCM clustering comparing to the traditional GA-FCM algorithm and PSOFCM algorithm. It proved that the algorithm in this paper can improve the FCM clustering effectively. Though GA-FCM, PSO-FCM provide better segmentation there exist obvious misclassification Pixels. Visually, the proposed method achieves the better result, over K-Means, FCM, FFCM, GA-FCM and PSO-FCM. Similarly Fig.3, Fig.4 and Fig.5 achieves betters results.

5.1 Quantitative results:

Performance of different image segmentation algorithm can be compared with following parameters:

True Positive (TP): Both proposed segmentation algorithm and Ground Truth(GT) are positive
True Negative (TN): Both proposed segmentation algorithm and Ground Truth(GT) are negative
False Positive (FP): Proposed segmentation algorithm result is positive and Ground Truth(GT) are negative.
False Negative (FN): Proposed segmentation algorithm result is negative and Ground Truth(GT) is positive.

Dice: $2(TP+TN)/(P+N+\hat{P}+\hat{N})$

PPV: $TP/(TP+FP)$

Sensitivity = $TP / (TP+FN)$

Where P to the real positives of the ground truth, N to the real negatives of the ground truth, $\hat{P}$ to the estimated positives of the proposed segmentation, $\hat{N}$ to the estimated negatives of the proposed segmentation. antitative results from table 1, gives better results than the existing methods.

Table 1. Summary of average results obtained by different unsupervised algorithms

Algorithm	**Dice**			**PPV**			**Sensitivity**		
	complete	**core**	**enhancing**	**complete**	**core**	**enhancing**	**complete**	**core**	**enhancing**
K-Means	0.68	0.49	0.53	0.71	0.44	0.65	0.71	0.55	0.49
FCM	0.71	0.51	0.42	0.65	0.46	0.38	0.73	0.58	0.41
FFCM	0.71	0.49	0.56	0.66	0.51	0.64	0.76	0.62	0.52
GA-FCM	0.72	0.54	0.58	0.68	0.57	0.61	0.74	0.64	0.57
PSO-FCM	0.73	0.53	0.59	0.68	0.58	0.63	0.76	0.60	0.55
OBL-GA FCM	**0.79**	**0.58**	**0.57**	**0.68**	**0.59**	**0.66**	**0.79**	**0.68**	**0.57**

5.2 Computational Cost:

Table2 Comparison in number of iterations

	FCM	**FFCM**	**GA-FCM**	**PSO-FCM**	**OBL-GA FCM**
DS1	90	84	52	39	**28**
DS2	63	42	34	28	**19**
DS3	74	61	53	48	**21**
DS4	100	100	86	78	**47**

Figure 1: Comparison in number of iterations

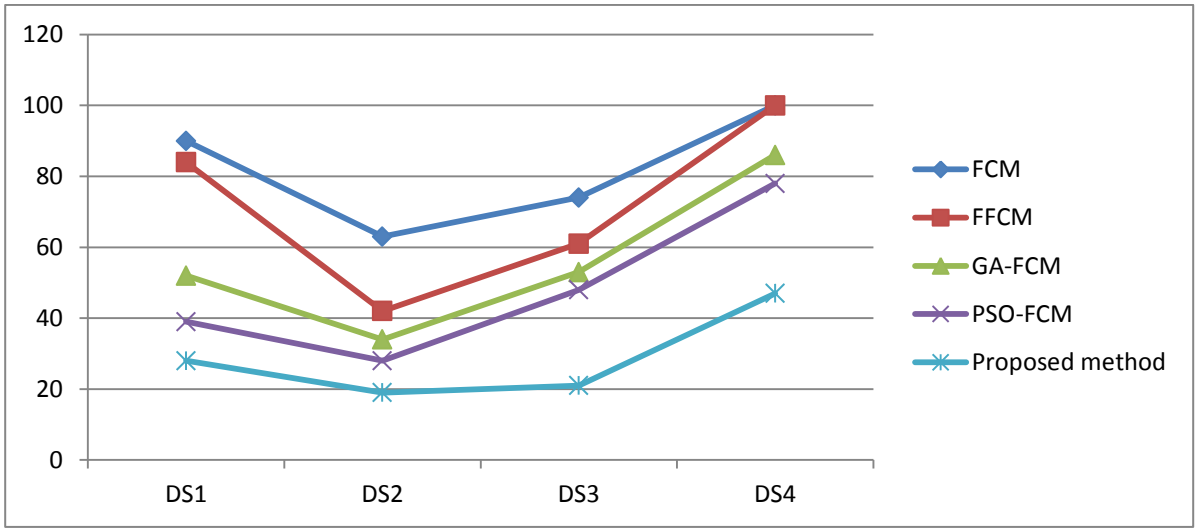


Fig 2.(a) Original Image	Fig 2.(b) K-Means	Fig 2.(c) FCM	Fig.2(d) FFCM

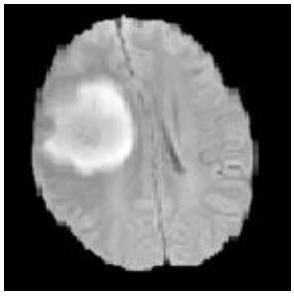
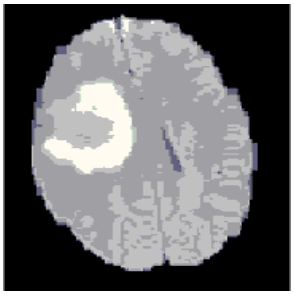
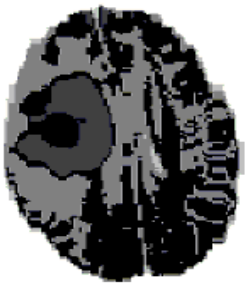
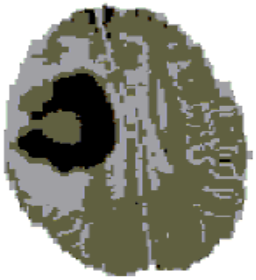

			

Fig 2.(e) GA-FCM	Fig 2.(f) PSO-FCM	Fig 2.(g) Proposed method	Fig 2.(h) Proposed method with level sets
			
Fig 3.(a) Original Image	Fig 3.(b) K-Means	Fig 3.(c) FCM	Fig.3(d) FFCM

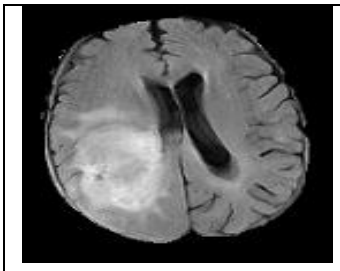


Fig 3.(e) GA-FCM

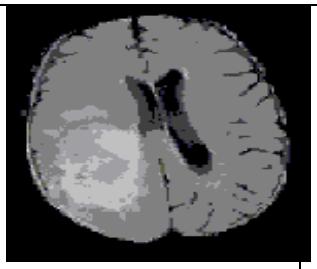


Fig 3.(f) PSO-FCM

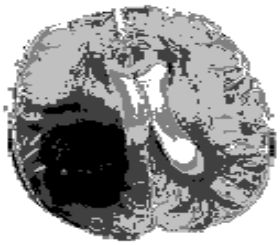


Fig 3.(g) Proposed method

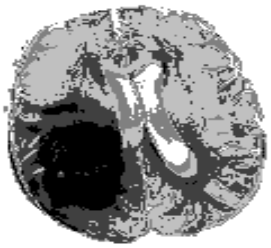
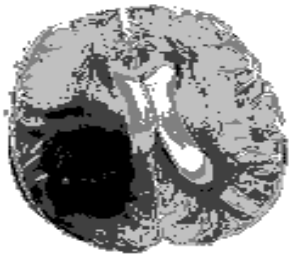


Fig 3.(h) Proposed method with level sets



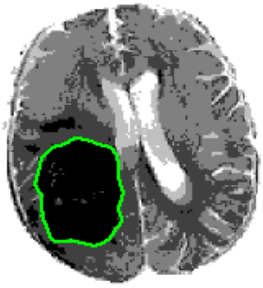


Fig 4.(a) Original Image

Fig 4.(b) K-Means

Fig 4.(c) FCM

Fig.4(d) FFCM

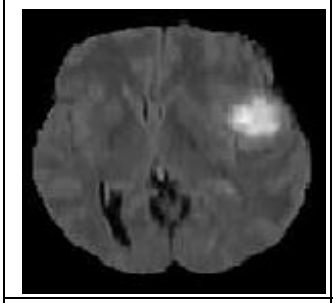


Fig 4.(e) GA-FCM

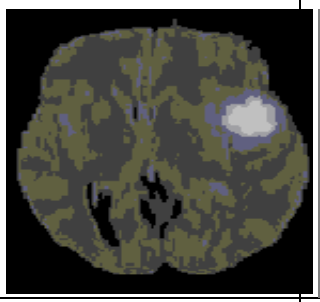


Fig 4.(f) PSO-FCM

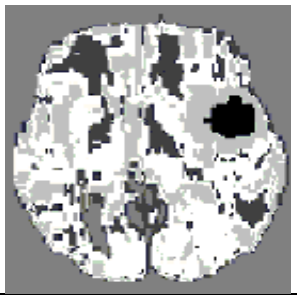
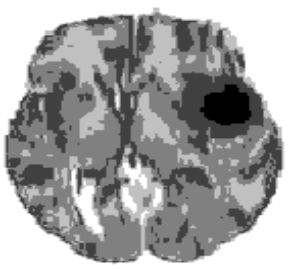


Fig 4.(g) Proposed method

Fig 4.(h) Proposed method with level sets



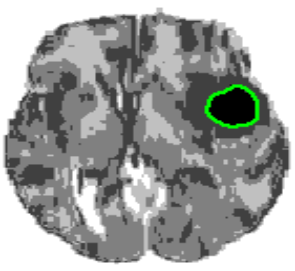


Fig 5. (a) Original Image

Fig 5.(b) K-Means

Fig 5.(c) FCM

Fig.5(d) FFCM

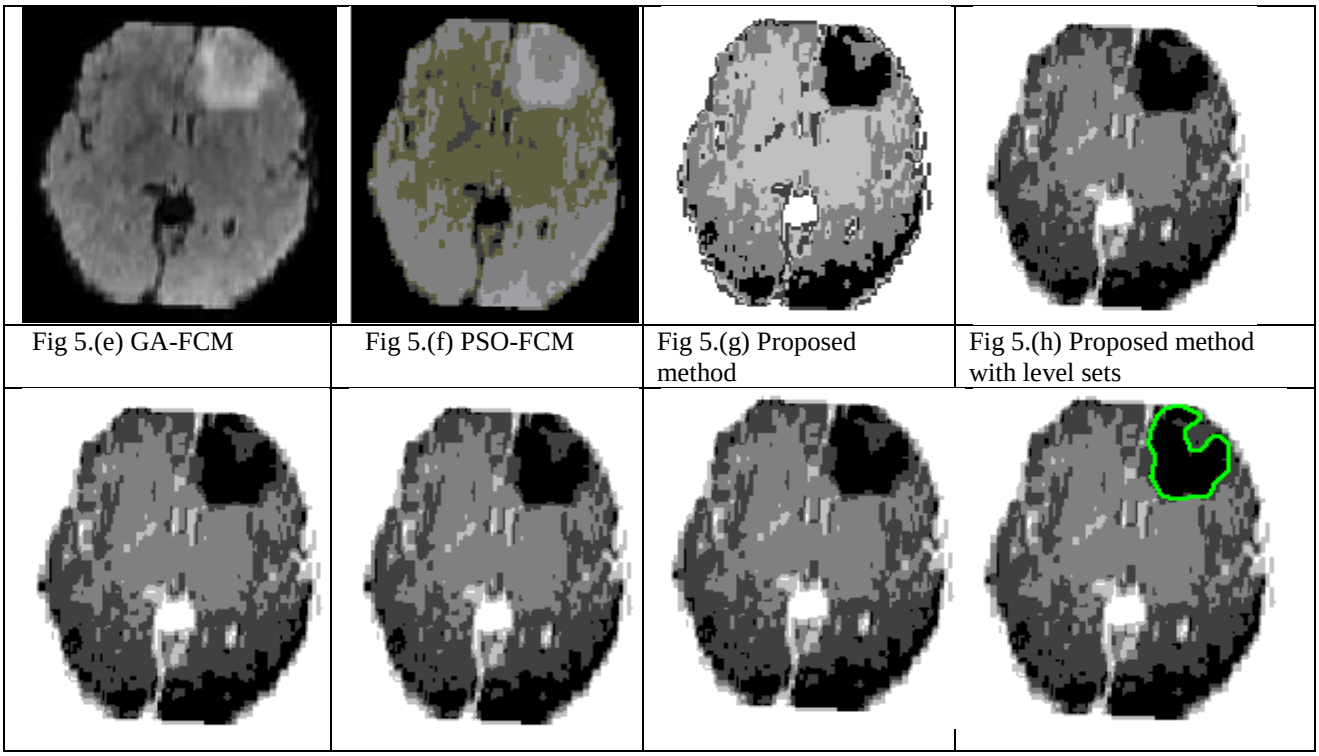


Fig 5.(e) GA-FCM | Fig 5.(f) PSO-FCM | Fig 5.(g) Proposed method | Fig 5.(h) Proposed method with level sets

V1. CONCLUSION

In this work, OBL-GA based FCM clustering algorithm with level sets is proposed. It overcomes the shortcoming of traditional GA's easy to be premature by introducing the OBL mechanism into GA. And then applying the OBL-GA algorithm to the fuzzy clustering algorithm, which improve the effect of fuzzy clustering by using its powerful global optimization ability. The proposed method is tested on Brain Tumor Image Segmentation (BRATS) Benchmark dataset. The tumor segmentation result will depend on both the histopathological properties of the Glioblastoma Multiforme and the characteristics revealed in the MR image. After processing of all the images by K-means, conventional FCM, FFCM, GA-FCM, PSO-FCM. We found both false positives and false negatives errors in the comparison between the segmented image and the ground truth. The false negative errors correspond to areas with weak or intermediate contrast enhancement in the tumor boundary. In this sense, OBL-GA FCM was better to include these areas. From the experimental results, we proved the effectiveness of our approach qualitatively and quantitatively in GBM tumor segmentation by comparing with other state of art methods.

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